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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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| model   |
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| nsing   |
| search, |
| protein |
| 1       |
| protein |
| ĕ       |

May 8, 2002, 11:07:10 ; Search time 19.51 Seconds
(without alignments)
2077.133 Million cell updates/sec Run on:

US-09-911-513-2

2758 1 MKRDHHHHHQDKKTMMMNEE.....MLGWHTRPLIATSAWKLSTN 532 Perfect score: Sequence: Scoring table:

219241 segs, 76174552 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 st

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |        |                |                       |     | SUMMARIES |                    |
|---------------|--------|----------------|-----------------------|-----|-----------|--------------------|
|               |        | æ              |                       |     |           |                    |
| Result<br>No. | Score  | Query<br>Match | Query<br>Match Length | DB  | ID        | Description        |
| 1             | 2747.5 | 9.66           | 533                   | . 7 | H86282    | protein F10B6.34 [ |
| 7             | 2185.5 | 79.2           | 587                   | ~   | D84426    | hypothetical prote |
| ٣             | 1587   | 57.5           | 511                   | 7   | G96688    | hypothetical prote |
| 4             | 1490   | 54.0           | 523                   | 7   | T51475    | RGA-like protein - |
| 5             | 602.5  |                | 653                   | 7   | T47581    | SCARECROW1 - Arabi |
| 9             | 598.5  | 21.7           | 653                   | 7   | T51244    | SCARECROW protein  |
| 7             | 588.5  | 21,3           |                       | ~   | D96656    | hypothetical prote |
| 80            | 565.5  | 20.5           |                       | 7   | E96540    | hypothetical prote |
| σ             | 564    | 20.4           |                       | ~   | G84462    | probable SCARECROW |
| 10            | 562.5  | 20.4           |                       | 7   | E96542    | scarecrow-like pro |
| 11            | 531.5  | 19.3           |                       | 7   | T51242    | Scll protein (impo |
| 12            | 506.5  | 18.4           |                       | 7   | T51236    | scarecrow-like pro |
| 13            | 487.5  | 17.7           |                       | 7   | E86347    | hypothetical prote |
| 14            | 453.5  | 16.4           |                       | 7   | T51232    | scarecrow-like pro |
| 15            | 451.5  | 16.4           |                       | 7   | T51234    | scarecrow-like pro |
| 16            | 440    | 16.0           | _                     | ~   | T02736    | probable SCARECROW |
| 17            | 431    | 15.6           |                       | 7   | T51241    | scarecrow-like pro |
| 18            | 429    | 15.6           | 375                   | 7   | C71441    | probable SCARECROW |
| 19            | 428    | 15.5           |                       | 7   | T45597    | scarecrow-like pro |
| 20            | 422.5  | 15.3           |                       | 7   | T46142    | scarecrow-like 7 ( |
| 21            | 412    | 14.9           |                       | ~   | T51235    | scarecrow-like pro |
| 22            | 407    | 14.8           | 718                   | 7   | T02531    | probable SCARECROW |
| 23            | 393.5  | 14.3           | 531                   | 7   | T04722    | hypothetical prote |
| 24            | 389.5  | 14.1           | 573                   | 7   | T51239    | scarecrow-like pro |
| 25            | 378.5  | 13.7           | 483                   | 7   | T10552    | hypothetical prote |
| 26            | 336    | 12.2           | 558                   | 7   | T01343    |                    |
| 27            | 335.5  | 12.2           | 378                   | 7   | T51237    |                    |
| 28            | 326    | 11.8           | 640                   | 7   | B84887    | probable SCARECROW |
| 29            | 320.5  | 11.6           | 410                   | 7   | T45848    | hypothetical prote |

| scarecrow-like pro | SCARECROW-like pro | scarecrow-like pro | scarecrow-like pro | Scll protein [impo | syringomycin synth | mycosubtilin synth | transcription fact | hevin precursor - | acyl-CoA oxidase h | scarecrow-like pro | condensin complex | hypothetical prote | probable membrane | hypothetical prote | genome polyprotein |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|
| T47874             | E85433             | T51233             | T51240             | T51243             | T14593             | T44806             | A55004             | S60062            | T04480             | T51238             | T43519            | T47905             | S54471            | T26135             | GNVSPV             |
| 7                  | ~                  | 7                  | 7                  | 7                  | 7                  | 7                  | ~                  | ~                 | 7                  | 7                  | 7                 | ~                  | 7                 | 7                  | т                  |
| 623                | 486                | 205                | 133                | 261                | 9376               | 3971               | 772                | 664               | 275                | 112                | 1158              | 673                | 1420              | 1829               | 3206               |
| 11.1               | 6.6                | 8.2                | 6.7                | 9.9                | 4.3                | 4.2                | 4.1                | 4.0               | 3.9                | 3.9                | 3.9               | 3.9                | 3.9               | 3.8                | 3.8                |
| 306.5              | 272                | 225                | 185                | 183                | 118                | 116.5              | 112.5              | 110.5             | 108                | 107                | 107               | 106.5              | 106.5             | 106                | 106                |
| 30                 | 31                 | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                | 39                 | 40                 | 41                | 42                 | 43                | 44                 | 45                 |
|                    |                    |                    |                    |                    |                    |                    |                    |                   |                    |                    |                   |                    |                   |                    |                    |

## ALIGNMENTS

| RESULT 1<br>H86282  |
|---|
| protein F10B6.34 [imported] - Arabidopsis thaliana<br>C;Species: Arabidopsis thaliana (mouse-ear cress)<br>C;Date: 07-Mars2001 #socious convision 02-Mars2001 |
| C. Accession: 186282  |
| R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon   |
| Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Huches, B.; Huizar, L.                                       |
| Nature 408, 816-820, 2000   |
| A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  |
| C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia   |
| Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.   |
| A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall   |
| ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  |
| A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.   |
| A; Reference number: A86141; MUID:21016719  |
| A; Accession: H86282  |
| A;Status: preliminary   |
| A; Molecule type: DNA   |
| A; Residues: 1-533 <sto></sto>  |
| A; Cross-references: GB:AE005172; NID:g8778219; PIDN:AAF79228.1; GSPDB:GN00141  |
| C;Genetics:   |
| A; Gene: F10B6.34   |
| A;Map position: 1   |
|   |
| Query Match 99.6%; Score 2747.5; DB 2; Length 533;  |
| 1ve (   |
| 210000000000000000000000000000000000000   |

60 QEDDLSQLATETVHYNPAELYTWLDSMLTDLNPPSSNAEYDLKAIPGDAILNQFAIDSAS 119 QEDDLSQLATETVHYNPAELYTWLDSMLTDLNPPSSNAEYDLKAIPGDAILNQFAIDSAS 120

61

1 MKRD-HHHHHQDKKTMMMNEEDDGNGMDELLAVLGYKVRSSEMADVAQKLEQLEVMMSNV 59

ò g Qy рp δy QQ δ qq δ qq δ

us-09-911-513-2.rpr

| OY 420 VSTLFDSLEGVPSGQDKVWSEVYLGKQICNUVACDGDDRVERHETLSQWRNRFGSSGFAA 479   | Ouery Match  Ouery Match  Best Local Similarity  Ouery Match  Best Local Similarity  Ouery Match  Best Local Similarity  Ouery Match  Matches 139; Conservative  In the conservative of th |
|---|--|
| Db 301 FRLTGIGPPAPDNFDYLHEVGCKLAHLAEAIHVEFEYRGFVANTLADLDASMLELRPSEI 360  Qy 360 ESVAVNSVPELHKLIGRPCAIDVLGVVNQTRPEIFTVVEOESNHNSPIFLDRFTESLHY 419  1111111111111111111111111111111111 | OUETY Match  Best Local Similarity 74.38; Prof. No. 6.8e-155;  Best Local Similarity 74.38; Prof. No. 6.8e-155;  Matches 440; Conservative 39; Mismatches 44; Indels 69; Gaps 9;  OY 1 MARDHHHHHODKTWAMMEEDEDGRAM-DELLAVIGTKVRSEBA 43    III   |

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Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia kano, H.
J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo omosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                           J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon onway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                         10092507; PIDN: AAG12907.1; GSPDB:GN00141
                                                                                                                                                                  ed] - Arabidopsis thaliana
9-ear cress)
02-Mar-2001 #text_change 31-Mar-2001
AVSQIGAMRKVATYFAEALARRIYRLSPSGSP 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IEVGCKLAHLAEAIHVEFEYRGFVANTLADLDA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSMLTDLNP----PSSNAEYDLKAIPGDAILN 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSNGVVETTTATAESTRHVVLVDSQENGVRLV 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              re 1587; DB 2; Length 511;
1. No. 2.2e-110;
fismatches 104; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGMDELLAVLGYKVRSSEMADVAQKLEQLEVM 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:|||| ||||||||||::
AGVDELLVVLGYKVRSSDMADVAHKLEQLEMV
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N.Alternate names: protein F24B22.180
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 20.Apr-2000 #sequence_revision 20.Apr-2000 #text_change 20.Apr-2000
C.Accession: T47581
R.Bloecker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, submitted to the Protein Sequence Database, January 2000
A; Reference number: 223016
A; Accession: T47581
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 1::: :111: 1::: :1112 PCNPNLGALLEYRLKSL------MLLDPSSSSDPSPQTFEPLYQISNNPSPPQQQQQH 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QENGVRLVHALLACAEAVQKENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARR-- 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----IYRLSPSQ-SPIDHSLS--DTLQMHFYETCPYLKFAHFTANQAILEAFQGKKRVH 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272 VIDFSMSQGLQWPALMQALALRPGGPPVFRLTGIGPPAPDNFDYLHEVGCKLAHLAEAIH 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEIFTVVEQESNHNSPIFLDRFTESLHYYSTLFDSL---EGVPSGQDKVMSEVYLGKQIC 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 VEFEYRGFVANTLADLDASMLELRPSEIESVAVNSVFELHKLLGRPGAIDKVLGVVNQIK 391
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           - 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----- QGGGGDTYTTNKRLKCSNGVVETTTATA--ESTRHVVLVDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 QQQQQQHKPPPPPIQQQERENSSTDAPPQPETVTATVPAVQTNTAEALRERKEEIKRQKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVVACDGPDRVERHETLSQWRNRFGSAGFAAAHIGSNAFKQASMLLALFNGGEGYRVEES
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                              A;Molecule type: DNA'
A;Residues: 1-653 <BLO>
A;Cross-references: EMBL:AL132957
A;Experimental source: cultivar Columbia; BAC clone F24B22
                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 VMMS--NVQEDDLSQLATETVHYNPAELYTWLDSMLTDLNPPSSNA-
                                                                                                                                                                                                                                                                                                                                                                                                                           186;
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SCARECROW protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                           21.8%; Score 602.5; Dl
30.9%; Pred. No. 7e-37
iive 85; Mismatches
                                                                     - Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                             A; Map position: 3
A; Introns: 511/2
A; Note: F24B22.180
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Simi
Matches 173;
                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                     SCARECROWI
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                                                                                                                                                                                                                                                              E.; Kotani, H.; Tabata,
                                                                                                                                                                       RGA-11ke protein - Arabidopsis thaliana
N;Alternate names: protein R3M16_60
C;Speciaes: Arabidopsis thaliana (mouse-ear cress)
C;Speciaes: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: T51475
R;Sato, S; Nakamura, Y; Kaneko, T; Kato, T; Asamizu, E.; Kotani, H.; Tabata, submitted to the Protein Sequence Database, August 2000
A;Reference number: 225394
A;Accession: T51475
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-523 <SAT>
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A;Residues: 1-523 <SAT>
A;Cross-references: EMBL:AL391150
A;Experimental source: cultivar Columbia; BAC clone K3M16
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 WVLSN----DIASSSNAFNDTVHYNPSDLSGWAQSMLSDLNYYPDLDPNRICDLRPITDD 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 HPSAAAIDPSFEEILQMNFYDSCPYLKFAHFTANQAILEAVTTSRVHVIDLGLNGGMQW 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 AILNQFAIDSASSSNQGGGGDTYTTNKRLK----CSNGVVETTTATAESTRHVVLVDSQE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HNSPIFLDRFTESLHYYSTLFDSLEG---VPSGQDKVMSEVYLGKQICNVVACDGPDRVE 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 VMMSNVQEDDL---SQLATETVHYNPAELYTWLDSMLTDLN---PPSSNAEYDLKAIPGD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKRDHHHHHQDKKTMMMNEE-DDGNG-----MDELLAVLGYKVRSSEMADVAQKLEQLE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LADLDASMLELRPSEIESVAVNSVFELHKLLGRPCAIDKVLGVVNQIKPEIFTVVEQESN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RHETLSQWRNRFGSAGFAAAHIGSNAFKQASMLLALFNGGEGYRVEESDGCLMLGWHTRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.0%; Score 1490; DB 2; 57.3%; Pred. No. 3.8e-103; ive 78; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 57,3
Matches 315; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||| ||||:
509 LIAASAWKLA 518
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A; Note: K3M16_60
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N 508
                                                                 s 530
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                                                                 530
                                                                                              508
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A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: D96656
A;Status: prellminary
A;Molecule type: DNA
A;Residues: 1-658 cSTO-
A;Cross-references: GB:AE005173; NID:g6598840; PIDN:AAF18695.1; GSPDB:GN00141
A;Gene: F16M19.21
A;Map position: 1
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Matches 166; Conservative
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R;Theologis, A.; Ecker, J.R.; Pealm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Cflin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunder, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, X.; Liu, S.X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
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C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000 C;Accession: T51244 R;di Laurenzio, L.; Wysocka-Diller, J.; Malamy, J.E.; Pvsh, L.; Helarintta.
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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                                  C; Accession: T51244
R; di Laurenzio, L.; Wysocka-Diller, J.; Malamy, J.E.; Pysh, L.; submitted to the EMBL Data Library, July 1996
A; Reference number: Z25338
A; Accession: T51244
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-653 CDLS
A; Cross-references: EMBL:U62798; PIDN:AAB06318.1
C; Genetics:
A; Gene: SCARECROW1
A; Introns: 511/2
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Pred. No. 1.4e-36;
; Mismatches 187;
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30.8%;
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Molecule type: DNA
Residues: 1-526 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable SCARECROW gene regulator [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: 684462
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
Ruir, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
Nature 402, 761-768, 1999
A;Tille: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Status: preliminary
                                                                                                                                                                                 11;
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            A Molecule type: DNA
A; Residues: 1-482 <STO>
A; Cross-references: GB: AE005173; NID: 99454566; PIDN: AAF97889.1; GSPDB: GN00141
C; Genetics:
A; Gene: F11F12.22
A; Map position: 1
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A;Residues: 1-413 <STO>
A;Cross-references: GB:AE002093; NID:g4585920; PIDN:AAD25580.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g04890
                                                                                                                                                                                                                                                                                                  256 ANQAILEAFQGKKRVHVIDFSMSQGLQWPALMQALALRPGGPPVFRLTGIGPPAPDNFDY 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323 LPSSGRTDSFLNAIWGLSPKVMVVTEQDSDHNGSTLMERLLESLYTYAALFDCLETKVPR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGQDKVMSEVYL-GKQICNVVACDGPDRVERHETLSQWRNRFGSAGFAAAHIGSNAFKQA 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRKVATYFAEALARRI----YRLSPSQSPIDHSLSDTLQMH--FYETCPYLKFAHFT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                 147 TATAESTRHVVLVD--SQENGVRLVHALLACAEAVQKENLTVAEALVKQIGFLAVSQIGA 204
                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                               316 LHEVGCKLAHLAEAIHVEFEYRGFVANTLADLDASMLE-LRPSEIESVAVNSVFELHKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 ASDDDLMRKNCALRFQNNPSGVDLQRVLMMSHGSAAEARENDMSNNNGYSPSGDSASSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 --RPGAIDKVLGVVNQIKPEIFTVVEQESNHNSPIFLDRFTESLHYYSTLFDSLE-GVP-
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                                                                                                                                                Length 482;
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                                                                                                                                             20.5%; Score 565.5; DB 2; 31.7%; Pred. No. 2.5e-34; iive 72; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.4%; Score 564; DB 2; Le 34.1%; Pred. No. 2.6e-34; ive 90; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491 SMLLALFNGGEGYRVEESDGCLMLGWHTRPLIATSAWK 528
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Best Local Similarity 31.75
Matches 145; Conservative
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Best Local Similarity 34.11
Matches 133; Conservative
A;Status: preliminary
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A; Map position: 2
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156 VVLVDSQENG-VRLVHALLACAEAVQKENLTVAEALVKQI-GFLAVSQIGAMRKVATYFA 213

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Scarccrow-like protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: E96542
C;Accession: E96542
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Highes, B.; Huizar, L.
Nature 408, B16-820, 2000
A;Authors: Huizar, L.
Nature, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Mairzla Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Recension: E96542
A;Recession: E96542
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A;Gene: F1756.12
A;Map position: 1
                                                                                                                                             381
                                                                                                                                                                                                                                                                                                                                                                                                                                    265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : : : | :: | :: | :: | :: | :: | 326 EQHCMARDVVNIIACEGAERIERHELLGKWKSRFSMAGFEPYPLSS--IISATIRALLRD 383
                                                                                                                                                                                                                                   GKKRVHVIDFSMSQGLQWPALMQALALRPGGPPVFRLTGIGPPAPDNFDYLHEVGCKLAH 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382 KVLGVVNQIKPEIFTVVEQESNHNSPIFLDRFTESLHYYSTLFDSLEGV--PSGQDKVMS 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 QEDDLSQLA-TETVHYNPAELYTWLDSMLTDLNPPSSNAEYDLKAIPGDAILNQFAIDSA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSSNQGGGGDTYTTNKRLKCSNGVVETTTATAESTRHVVLVDSQENGVRLVHALLACAEA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --NNQGGFGQ------QHGVV--SSAMYRSMEMISRGD------LKGVLYECAKA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 HSLSDTLOMH-FYETCPYLKFAHFTANQAILEAFQGKKRVHVIDFSMSQGLOWPALMQAL 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :::|:: | ::|| |:|||:|||:|| : || ::: | :::: |
LLIVEAISRGDLKLV--LVACAKAVSENNLLMARWCMGELRGMVSISG-EPIORLGAYML 95
                                                                                                                                                                                                                                                                            LAEAIHVEFEYRGFVANTLADLDASMLELRPSEIESVAVNSVFELHKL----LGRPGAID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVY-LGKQICNVVACDGPDRVERHETLSQWRNRFGSAGFAAAHIGSNAFKQASMLLALFN
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                                                                                                   EALARR-----IYRLSPSQSPIDHS-LSDTLQMHFYETCPYLKFAHFTANQAILEAFQ
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Best Local Similarity 31.89
Matches 155; Conservative
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Indels

Length 306;

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468 248

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hypothetical protein AAF87898.1 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hudpes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Yi, Lin, X.; Liu, X.X.; Liu, Z.A.; Luros, J.S.; Malti, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, X.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A;Reference number: A86141; MuID:21016719
A;Cross-references: GB:AE005172; NID:99454575; PIDN:AAF87898.1; GSPDB:GN00141 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 MH-FYETCPYLKFAHFTANQAILEAFQGKKRVHVIDFSMSQGLQWPALMQALALRPGGPP 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                           469 RNRFGSAGFAAAHIGSNAFKQASMLLALFNGGEGYRVEESDGCLMLGWHTRPLIATSAWK 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEYDLKAIPGDAILNQFAIDSASSSNQGGGDTYTTNKRLKCSNGVVETTTATAESTRHV 156
                                                                                                                                                                                                                                                                                                                                                                             299 VFRLTGIGPPAPD--NFDYLHEVGCKLAHLAEAIHVEFEYRGFVANTLADLDASMLELRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEIESVAVNSVFELHKLLGRPGAI - - - - DKVLGVVNQIKPEIFTVVEQESNHNSPIFLDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTESLHYYSTLFDSLEGVPSGQD----KVMSEVY-LGKQICNVVACDGPDRVERHETLSQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 VRSSEMADVAQKLEQLEVMMSNVQEDDLSQLATETVHYNPAELYTWLDSMLTDLNPPSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 593;
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                                                                                                                                                                                                                                                                                                               108;
                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                       18.4%; Score 506.5; DB 2
llarity 39.0%; Pred. No. 3.1e-30;
Conservative 58; Mismatches 108
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                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 117; Conserv
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Matches 145; Conserv
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A; Residues: 1-593 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Zea mays (maize)
C;Species: Zea mays (maize)
C;Species: Zea mays (maize)
C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000
C;Accession: T51242
A;Title: The GRAS gene family in Arabidopsis: sequence characterization and basic expres
A;Reference number: Z5337; MUID:99272994
A;Reference number: Z5337; MUID:99272994
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-313 <PYS-
A;Cross-references: EMBL:AF067400; PIDN:AAC98090.1
C;Genetics:
A;Gene: SC11
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000
C;Accession: T51236
                                                                                                                                                                                                                                   NSPIFLDRFTESLHYYSTLFDSLEGVPSGQD---KVMSEVY-LGKQICNVVACDGPDRVE 460
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                                                                                                                                                                                                                                                                                          RHETLSOWRNRFGSAGFAAAHIGSNAFKQASMLLALFNGGEGYRVEESDGCLMLGWHTRP
      PEL--LTYMHILYEACPYFKFGYESANGAIAEAVKNESFVHIIDFQISQGGQWVSLIRAL
                                              291 ALRPGGPPVFRLTGIGPPAPD -- NFDYLHEVGCKLAHLAEAIHVEFEYRGFVANTLADLD
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Pred. No. 4.5e-32;
45; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMLLALFNGGEGYRVEESDGCLMLGWHTRPLIATSAW 527
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Best Local Similarity
Matches 116; Conserv
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19;

Gaps

83;

| Db 496 SSKKTSAADMLKAYQTYMSVCPFKKAAIIFANHSMARFTANANTIHIIDFGISYGFG 216 217 218 270 283 WPALMQALAL-RPGGPPVFRLTGIGPPAPDNFDYLHEVGCKLAHLAEAIHVEFEYRGF 1 | •  | basic expres   | 9y 241<br>pps 21;   | 392 Qy 415 171 Db 237 435 Qy 472 224 Db 297 495 Qy 525 282 |
|---|--|--|---|--|
|   | OY 440 EVYLGKQICNVVACDGPDRVERHETLSQWRNRFGSAGFAAAHIGSNAFKQASM 492   :     :     :     : | A;TILE: The GAKS gene family in Arabidopsis: sequence Characterizatia A;Reference number: 225337; MUID:99272994 A;Reference number: 225337; MUID:99272994 A;Retus: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-808 <pys> A;Cross-references: EMBL:AF036309; PIDN:AAD24412.1 A;Gene:SCL14</pys> | atch cal Similarity 25.8%; Score 453.5; DB 2; Length 808; 151; Conservative 91; Mismatches 185; Indels 159; DHHHHHQ | 365YVEESELSEM  |

Search completed: May 8, 2002, 11:10:39 Job time: 209 sec